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JUL 2001

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/330,235

DATE: 06/20/2001

TIME: 10:51:38

Input Set : A:\MOCO.156.00US.SeqListing.4jun01.txt

Output Set: N:\CRF3\06202001\I330235.raw

ENTERED

#17/16
3/16/01
6/20/01

3 <110> APPLICANT: Knutzon, Debbie
 5 <120> TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
 7 <130> FILE REFERENCE: MOCO.156.00US
 9 <140> CURRENT APPLICATION NUMBER: 09/330,235
 10 <141> CURRENT FILING DATE: 1999-06-10
 12 <150> PRIOR APPLICATION NUMBER: 60/089,043
 13 <151> PRIOR FILING DATE: 1998-06-12
 15 <160> NUMBER OF SEQ ID NOS: 22
 17 <170> SOFTWARE: PatentIn version 3.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1391
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Caenorhabditis elegans
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 29 gtgaatgcaa acactaaaca ggccaccact gaagagccac gcattccaatt accaactgtg 180
 31 gatgctttcc gtcgtgcaat tccagcacac tgtttcgaaa gagatctcgt taaatcaatc 240
 33 agatatttgg tgcaagactt tgcggcactc acaattctct actttgctct tccagctttt 300
 35 gagtactttg gattgtttgg ttacttggtt tggaacattt ttatgggagt ttttggattc 360
 37 gcgttggtcg tcgttggaac cgattgtctt catggatcat tctctgataa tcagaatctc 420
 39 aatgatttca ttggacatat cgccttctca ccactcttct ctccatactt cccatggcag 480
 41 aaaagtcaca agcttcacca tgctttcacc aaccacattg acaaagatca tggacacgtg 540
 43 tggattcagg ataaggattg ggaagcaatg ccatcatgga aaagatgggt caatccaatt 600
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 47 tctcacttct ggccatactc ttactttttt gttcgtaact ctgaccgtgt tcaatgtgta 720
 49 atctctggaa tctgttgctg tgtgtgtgca tatattgctc taacaattgc tggatcatat 780
 51 tccaattggt tctggtacta ttgggttcca ctttctttct tcggattgat gctcgtcatt 840
 53 gttacctatt tgcaacatgt cgatgatgtc gctgagggtg acgaggctga tgaatggagc 900
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 59 catctcatcg aagcaaccga aggtgtcaaa aaggtcttgg agccgttggt cgacacccaa 1080
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 63 aagctcgact atctcgttca caagaccgcc ggaatcatgc aattccgaac aactctcgag 1200
 65 gagaaggcaa aggccaagta aaagaatatc ccgtgccgtt ctagagtaca acaacaactt 1260
 67 ctgcgttttc accggttttg ctctaattgc aatttttctt tgttctatat atattttttt 1320
 69 gctttttaat tttattctct ctaaaaaact tctacttttc agtgcgttga atgcataaag 1380
 71 ccataactct t 1391
 74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 402
 76 <212> TYPE: PRT
 77 <213> ORGANISM: Caenorhabditis elegans
 79 <400> SEQUENCE: 2
 81 Met Val Ala His Ser Ser Glu Gly Leu Ser Ala Thr Ala Pro Val Thr
 82 1 5 10 15
 84 Gly Gly Asp Val Leu Val Asp Ala Arg Ala Ser Leu Glu Glu Lys Glu
 85 20 25 30

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87 Ala Pro Arg Asp Val Asn Ala Asn Thr Lys Gln Ala Thr Thr Glu Glu
88      35              40              45
90 Pro Arg Ile Gln Leu Pro Thr Val Asp Ala Phe Arg Arg Ala Ile Pro
91      50              55              60
93 Ala His Cys Phe Glu Arg Asp Leu Val Lys Ser Ile Arg Tyr Leu Val
94 65              70              75              80
96 Gln Asp Phe Ala Ala Leu Thr Ile Leu Tyr Phe Ala Leu Pro Ala Phe
97      85              90              95
99 Glu Tyr Phe Gly Leu Phe Gly Tyr Leu Val Trp Asn Ile Phe Met Gly
100      100              105              110
102 Val Phe Gly Phe Ala Leu Phe Val Val Gly His Asp Cys Leu His Gly
103      115              120              125
105 Ser Phe Ser Asp Asn Gln Asn Leu Asn Asp Phe Ile Gly His Ile Ala
106      130              135              140
108 Phe Ser Pro Leu Phe Ser Pro Tyr Phe Pro Trp Gln Lys Ser His Lys
109 145              150              155              160
111 Leu His His Ala Phe Thr Asn His Ile Asp Lys Asp His Gly His Val
112      165              170              175
114 Trp Ile Gln Asp Lys Asp Trp Glu Ala Met Pro Ser Trp Lys Arg Trp
115      180              185              190
117 Phe Asn Pro Ile Pro Phe Ser Gly Trp Leu Lys Trp Phe Pro Val Tyr
118      195              200              205
120 Thr Leu Phe Gly Phe Cys Asp Gly Ser His Phe Trp Pro Tyr Ser Ser
121      210              215              220
123 Leu Phe Val Arg Asn Ser Asp Arg Val Gln Cys Val Ile Ser Gly Ile
124 225              230              235              240
126 Cys Cys Cys Val Cys Ala Tyr Ile Ala Leu Thr Ile Ala Gly Ser Tyr
127      245              250              255
129 Ser Asn Trp Phe Trp Tyr Tyr Trp Val Pro Leu Ser Phe Phe Gly Leu
130      260              265              270
132 Met Leu Val Ile Val Thr Tyr Leu Gln His Val Asp Asp Val Ala Glu
133      275              280              285
135 Val Tyr Glu Ala Asp Glu Trp Ser Phe Val Arg Gly Gln Thr Gln Thr
136      290              295              300
138 Ile Asp Arg Tyr Tyr Gly Leu Gly Leu Asp Thr Thr Met His His Ile
139 305              310              315              320
141 Thr Asp Gly His Val Ala His His Phe Phe Asn Lys Ile Pro His Tyr
142      325              330              335
144 His Leu Ile Glu Ala Thr Glu Gly Val Lys Lys Val Leu Glu Pro Leu
145      340              345              350
147 Ser Asp Thr Gln Tyr Gly Tyr Lys Ser Gln Val Asn Tyr Asp Phe Phe
148      355              360              365
150 Ala Arg Phe Leu Trp Phe Asn Tyr Lys Leu Asp Tyr Leu Val His Lys
151      370              375              380
153 Thr Ala Gly Ile Met Gln Phe Arg Thr Thr Leu Glu Glu Lys Ala Lys
154 385              390              395              400
156 Ala Lys
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 41

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161 <212> TYPE: DNA
162 <213> ORGANISM: synthetic primer
164 <400> SEQUENCE: 3
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169 <211> LENGTH: 38
170 <212> TYPE: DNA
171 <213> ORGANISM: synthetic primer
173 <400> SEQUENCE: 4
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178 <211> LENGTH: 32
179 <212> TYPE: DNA
180 <213> ORGANISM: synthetic polylinker
182 <400> SEQUENCE: 5
183 tcgacctgca ggaagcttgc ggccgcggat cc 32
186 <210> SEQ ID NO: 6
187 <211> LENGTH: 32
188 <212> TYPE: DNA
189 <213> ORGANISM: synthetic polylinker
191 <400> SEQUENCE: 6
192 tcgaggatcc gggcccgcaa gcttctctgca gg 32
195 <210> SEQ ID NO: 7
196 <211> LENGTH: 1353
197 <212> TYPE: DNA
198 <213> ORGANISM: Brassica napus
200 <400> SEQUENCE: 7
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203 ctctgtccaa atctctctct ccagcgatgg ttgttgctat ggaccagcgc agcaatgtta 120
205 acggagattc cgggtgcccg aaggaagaag ggtttgatcc aagcgcacaa ccaccgttta 180
207 agatcggaga tataagggcg gcgattccta agcattgctg ggtgaagagt cctttgagat 240
209 ctatgagcta cgtcaccaga gacattttcg ccgtcgcggc tctggccatg gccgcctgt 300
211 attttgatag ctggttctct tggccactct actgggttgc ccaaggaacc cttttctggg 360
213 ccactctcgt tcttggccac gactgtggac atgggagttt ctacagacatt cctctgctga 420
215 acagtgtggt tggtcacatt cttcattcat tcactctcgt tccttaccat ggttggagaa 480
217 taagccatcg gacacaccac cagaaccatg gccatgttga aaacgacgag tcttgggttc 540
219 cgttgccaga aaagttgtac aagaacttgc cccatagtac tcggatgctc agatacactg 600
221 tccctctgcc catgctcgtt taccgatct atctgttgta cagaagtcct ggaaaagaag 660
223 ggtcacattt taaccatac agtagtttat ttgttccaag cgagaggaag cttattgcaa 720
225 cttcaactac ttgctggtcc ataagtgttg ccaactttgt ttatctatcg ttctcgttg 780
227 atccagtcac agttctcaaa gtctatggcg ttccttacat tatctttgtg atgtggttg 840
229 acgctgtcac gtacttgcat catcatggtc acgatgagaa gttgccttgg tacagaggca 900
231 aggaatggag ttattttacgt ggaggattaa caactattga tagagattac ggaatcttca 960
233 acaacatcca tcacgacatt ggaactcagc tgatccatca tcttttccca caaatccctc 1020
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237 agccgaagac gtcaggagca ataccgattc acttggttga gagtttggtc gcaagtatta 1140
239 aaaaagatca ttacgtcagt gacactggtg atattgtctt ctacgagaca gatccagatc 1200
241 tctacgttta tgcttctgac aaatctaaaa tcaattaact tttcttctta gctctattag 1260
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249 <211> LENGTH: 383
250 <212> TYPE: PRT
251 <213> ORGANISM: Brassica napus
253 <400> SEQUENCE: 8
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259 20 25 30
261 Ile Gly Asp Ile Arg Ala Ala Ile Pro Lys His Cys Trp Val Lys Ser
262 35 40 45
264 Pro Leu Arg Ser Met Ser Tyr Val Thr Arg Asp Ile Phe Ala Val Ala
265 50 55 60
267 Ala Leu Ala Met Ala Ala Val Tyr Phe Asp Ser Trp Phe Leu Trp Pro
268 65 70 75 80
270 Leu Tyr Trp Val Ala Gln Gly Thr Leu Phe Trp Ala Ile Phe Val Leu
271 85 90 95
273 Gly His Asp Cys Gly His Gly Ser Phe Ser Asp Ile Pro Leu Leu Asn
274 100 105 110
276 Ser Val Val Gly His Ile Leu His Ser Phe Ile Leu Val Pro Tyr His
277 115 120 125
279 Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn His Gly His Val
280 130 135 140
282 Glu Asn Asp Glu Ser Trp Val Pro Leu Pro Glu Lys Leu Tyr Lys Asn
283 145 150 155 160
285 Leu Pro His Ser Thr Arg Met Leu Arg Tyr Thr Val Pro Leu Pro Met
286 165 170 175
288 Leu Ala Tyr Pro Ile Tyr Leu Trp Tyr Arg Ser Pro Gly Lys Glu Gly
289 180 185 190
291 Ser His Phe Asn Pro Tyr Ser Ser Leu Phe Ala Pro Ser Glu Arg Lys
292 195 200 205
294 Leu Ile Ala Thr Ser Thr Thr Cys Trp Ser Ile Met Leu Ala Thr Leu
295 210 215 220
297 Val Tyr Leu Ser Phe Leu Val Asp Pro Val Thr Val Leu Lys Val Tyr
298 225 230 235 240
300 Gly Val Pro Tyr Ile Ile Phe Val Met Trp Leu Asp Ala Val Thr Tyr
301 245 250 255
303 Leu His His His Gly His Asp Glu Lys Leu Pro Trp Tyr Arg Gly Lys
304 260 265 270
306 Glu Trp Ser Tyr Leu Arg Gly Gly Leu Thr Thr Ile Asp Arg Asp Tyr
307 275 280 285
309 Gly Ile Phe Asn Asn Ile His His Asp Ile Gly Thr His Val Ile His
310 290 295 300
312 His Leu Phe Pro Gln Ile Pro His Tyr His Leu Val Asp Ala Thr Arg
313 305 310 315 320
315 Ala Ala Lys His Val Leu Gly Arg Tyr Tyr Arg Glu Pro Lys Thr Ser
316 325 330 335
318 Gly Ala Ile Pro Ile His Leu Val Glu Ser Leu Val Ala Ser Ile Lys

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319          340          345          350
321 Lys Asp His Tyr Val Ser Asp Thr Gly Asp Ile Val Phe Tyr Glu Thr
322          355          360          365
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325          370          375          380
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328 <211> LENGTH: 40
329 <212> TYPE: DNA
330 <213> ORGANISM: synthetic primer
332 <400> SEQUENCE: 9
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336 <210> SEQ ID NO: 10
337 <211> LENGTH: 37
338 <212> TYPE: DNA
339 <213> ORGANISM: synthetic primer
341 <400> SEQUENCE: 10
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346 <211> LENGTH: 1482
347 <212> TYPE: DNA
348 <213> ORGANISM: Mortierella alpina
350 <400> SEQUENCE: 11
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395 caaggatacg ttttggaag catttgcttc acatttggag cacttgctgt ttcttggaact 1380
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402 <210> SEQ ID NO: 12
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VERIFICATION SUMMARY

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